

Schreiber, David

887-66

From: Steadman, David (AU1652)
Sent: Monday, March 10, 2003 4:23 PM
To: Schreiber, David
Subject: 09/991,212 sequence comparison

NAME: David Steadman
AU: 1652
Date: 03/10/03
Office: 10D-04
Mailbox: 10D-01

Mr. Schreiber, please compare the following sequences:

- 1) SEQ ID NO:1 against SEQ ID NO:5
- 2) SEQ ID NO:2 against SEQ ID NO:5

Please save results to diskette.

Thank you very much.

David J. Steadman
Art Unit 1652
Crystal Mall 1 Room 10D-04
703-308-3934

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>D. Schweiber</u>	NA Sequence (#) <u>2</u>	STN _____
Searcher Phone #: <u>308-4292</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: <u>CM1 CA03</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>3/11</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>18</u>	Fulltext _____	Sequence Systems <u>CompuGen GCS</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>26</u>	Other _____	Other (specify) _____

RESULT 7

HSZ83953
 LOCUS HSZ83953 570 bp mRNA linear PRI 16-JAN-1997
 DEFINITION H.sapiens mRNA; clone CD 274.
 ACCESSION Z83953
 VERSION Z83953.1 GI:1783342
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 570)
 AUTHORS Gasparini, P.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 570)
 AUTHORS Gasparini, P.
 TITLE Direct Submission
 JOURNAL Submitted (13-JAN-1997) Gasparini P., Servizio di Genetica Medica,
 I.R.C.C.S. - Ospedale CSS Viale Cappuccini, I-71013 San Giovanni
 Rotondo, Foggia, ITALY
 FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p22"
 /clone="CD 274"
 BASE COUNT 127 a 134 c 134 g 171 t 4 others
 ORIGIN

Query Match 18.0%; Score 296; DB 9; Length 570;
 Best Local Similarity 100.0%; Pred. No. 1.2e-155;
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  519 GTGGGGCCCTCCACAAGAACGAAGCAGACTCTGCAGCATTGCTTTATCAGGAATGTTACT 578
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Db  275 GTGGGGCCCTCCACAAGAACGAAGCAGACTCTGCAGCATTGCTTTATCAGGAATGTTACT 334

Qy  579 GGGATGCTTTACTGCCATCCTCATAGGTGGCTTCATTAGTGAAACCCTTGGGTGGCCCTT 638
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  335 GGGATGCTTTACTGCCATCCTCATAGGTGGCTTCATTAGTGAAACCCTTGGGTGGCCCTT 394

Qy  639 TGTCTTCTATATCTTTGGAGGTGTTGGCTGTGTCTGCTGCCTTCTCTGGTTGTTGTGAT 698
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Qy  699 TTATGATGACCCCGTTTCCTATCCATGGATAAGCACCTCAGAAAAAGAATACATCATATC 758
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  455 TTATGATGACCCCGTTTCCTATCCATGGATAAGCACCTCAGAAAAAGAATACATCATATC 514

Qy  759 CTCCTGAAACAACAGGTGCGGTCTTCTAAGCAGCCTCTTCCCATCAAAGCTATGC 814
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Db  515 CTCCTGAAACAACAGGTGCGGTCTTCTAAGCAGCCTCTTCCCATCAAAGCTATGC 570
  
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seq_documentation_block:

LOCUS HSZ83953 570 bp mRNA linear PRI 16-JAN-1997
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 AUTHORS Gasparini, P.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 570)
 AUTHORS Gasparini, P.
 TITLE Direct Submission
 JOURNAL Submitted (13-JAN-1997) Gasparini P., Servizio di Genetica Medica,
 I.R.C.C.S. - Ospedale CSS Viale Cappuccini, I-71013 San Giovanni
 Rotondo, Foggia, ITALY
 FEATURES Location/Qualifiers
 source 1..570
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p22"
 /clone="CD 274"
 BASE COUNT 127 a 134 c 134 g 171 t 4 others
 ORIGIN

alignment_scores:

Quality: 98.00 Length: 98
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-991-212A-1 x HSZ83953 ..

Align seg 1/1 to: HSZ83953 from: 1 to: 570

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  96 TrpGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSerGl 112
    |||
  276 TGGGGCCCTCCACAAGAACGAGCAGACTCTGCAGCATTGCTTTATCAGG 325

  112 yMetLeuLeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSerG 129
    |||
  326 AATGTACTGGGATGCTTTACTGCCATCCTCATAGGTGGCTTCATTAGTG 375

  129 luThrLeuGlyTrpProPheValPheTyrIlePheGlyGlyValGlyCys 145
    |||
  376 AAACCTTGGGTGGCCCTTTGTCTTCTATATCTTTGGAGGTGTTGGCTGT 425

  146 ValCysCysLeuLeuTrpPheValValIleTyrAspAspProValSerTy 162
    |||
  426 GTCTGCTGCCTTCTCTGGTTTGTGTGATTATGATGACCCCGTTTCCTA 475

  162 rProTrpIleSerThrSerGluLysGluTyrIleIleSerSerLeuLysG 179
    |||
  476 TCCATGGATAAGCACCTCAGAAAAAGAATACATCATATCTCCTTGAAAC 525

  179 lnGlnValGlySerSerLysGlnProLeuProIleLysAlaMet 193
    |||
  526 AACAGGTCGGGTCTTCTAAGCAGCCTCTTCCCATCAAAGCTATG 569

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-continued

(B) CLONE: XLR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTGATGCTC CCATGAGAAA ACTGG

25

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: XLF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGATTTTCG AGCATAGCAC CTGTC

25

What is claimed is:

1. An isolated and purified polynucleotide fragment encoding a polypeptide comprising the amino acid sequence of SEQ ID No:1.
2. A hybridization probe comprising the polynucleotide fragment of claim 1.
3. An isolated and purified polynucleotide fragment comprising SEQ ID No:2.
4. An isolated and purified polynucleotide fragment which is completely complementary to the polynucleotide of claim 1.
5. A hybridization probe comprising the polynucleotide fragment of claim 4.
6. An expression vector comprising the polynucleotide of claim 1.
7. A host cell containing the expression vector of claim 6.
8. A method for producing a polypeptide comprising the amino acid sequence of SEQ ID NO:1, the method comprising the steps of:
 - a) culturing the host cell of claim 7 under conditions suitable for the expression of the polypeptide; and
 - b) recovering the polypeptide from the host cell culture.
9. A method for detection of a polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:1 in a biological sample containing nucleic acid material, the method comprising the steps of:
 - a) hybridizing the polynucleotide of claim 4 to the nucleic acid material of the biological sample, thereby forming a hybridization complex; and
 - b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of the polynucleotide encoding the polypeptide in the biological sample.

* * * * *